

**AMENDMENTS TO THE CLAIMS**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims**

All pending claims are cancelled.

52. (New) A method of preparing a polypeptide by expressing at least one murine genomic region involved in the development of cancer, said genomic region being selected from the group consisting of: Adam11, AI462175, Cd24a, Edg3, Itgp, Kcnj16, Kcnk5, Kcnn4, Ly108, Ly6i, mouse homologue of EMILIN, Mrc1, Ninj2, Nphs1, Sema4b, Tm9sf2, and Tnfrsf17, encoding cell surface proteins; Apobec2, Btd, Cds2, Clpx, Ddx19, Ddx21, Dnmt2, Dqx1, Hdac7a, Lce-pending, Mgat1, mouse homologue of CILP, mouse homologue of NOH61, Nudel-pending, Pah, Pdi1, Ppia, Prps1, Ptgds, and Vars2, encoding enzymes; Dagk4, mouse homologue of PSK, Nme2, Snf1lk and Tyki, encoding kinases; Inpp4a and Inpp5b, encoding phosphatases; Il16, Prg, and Scya4, encoding secreted factors; Akap7, Api5, Arfrp1, Arhgap14-pending, Cish2, Dapp1, Fabp6, Fkbp8, Fliz1-pending, Hint, Ier5, Jundp2-pending, Lmo6, Mid1, mouse homologue of AKAP13, mouse homologue of BIN2, mouse homologue of CEZANNE, mouse homologue of CHD2, mouse homologue of MBLL, mouse homologue of SLC16A10, mouse homologue of SLC16A6, mouse homologue of SLC17A5, mouse homologue of TAF5L, mouse homologue of U1SNRNPBP, mouse homologue of ZNF8, Mtap7, Myo1c, Nkx2-3, Nsf, Pcdh9, Pkig, Prdx2, Pscd1, Psmb1, Psmel, Psme2, Rgl1, Ril-pending, Sax1, Slc14a2, Slc7a1, Slc7a11, Swap70, Txnip, and Ubl3, encoding signaling proteins; Clic3, Gtl1-13, mouse homologue of NOL5A, and Vdac2, encoding structural proteins; ABT1-pending, Ctbp1, Dermo1, Ebf, Elf4, Ldb1, mouse homologue of NR1D1, mouse homologue of ZER6, Rest, Tbp, Zfp238, Zfp287, and Zfp319, encoding proteins involved in transcriptional regulation; Lrrc2, Satb1, Slfn4, and genomic regions with the following Celera identification codes mCG10290, mCG10613, mCG11234, mCG11325, mCG11355, mCG11803, mCG11817, mCG12566, mCG12630, mCG12824, mCG13346, mCG14143, mCG14155, mCG14342, mCG15141, mCG15321,, mCG16761, mCG16858, mCG17127, mCG17140, mCG17142, mCG17547, mCG17569, mCG17751, mCG17799, mCG17802, mCG17918, mCG18034,, mCG1850, mCG18663, mCG18737,

mCG20276, mCG20905, mCG20994, mCG21403, mCG21505, mCG21529, mCG21530, mCG21803, mCG22014, mCG22045, mCG22386, mCG2258, mCG22772, mCG23032, mCG23035, mCG23069, mCG23075, mCG23120, mCG2543, mCG2824, mCG2947, mCG3038, mCG3729, mCG3760, mCG50409, mCG50651, mCG5068, mCG5070, mCG51393, mCG52252, mCG52498, mCG53009, mCG53724, mCG55023, mCG55075, mCG55198, mCG55265, mCG55512, mCG56069, mCG56089, mCG56746, mCG57132, mCG57265, mCG57617, mCG57827, mCG58254, mCG58345, mCG5900, mCG5905, mCG59368, mCG59375, mCG59533, mCG59662, mCG59810, mCG59997, mCG60526, mCG60833, mCG61221, mCG61661, mCG61897, mCG61907, mCG61943, mCG62177, mCG62971, mCG63537, mCG63601, mCG64346, mCG64382, mCG64398, mCG65022, mCG65585, mCG65785, mCG66128, mCG66379, mCG66776, mCG66965, mCG7831, mCG7856, mCG8424, mCG9002, mCG9537, mCG9538, mCG9791, mCG9792, mCG9843, mCG9875, mCG9877, and mCG988, or a human homologue thereof.

53. (New) A method of using at least one murine genomic region listed in claim 52 or its human homologue for the preparation of an inhibitor capable of inhibiting the transcription product or activity of a polypeptide encoded by said region or affected by transformations in said region, wherein said inhibitor is chosen from the group consisting of an antibody, an antisense molecule, an RNAi molecule, a ribozyme and a small molecule interfering with the biological activity of the polypeptide encoded by said genomic region or with the biological activity of a polypeptide the expression of which is affected by transformations in said genomic region.

54. (New) An isolated nucleic acid sequence comprising at least one murine genomic region listed in claim 52 or its human homologue, further comprising one or more regulatory sequences.

55. (New) A recombinant vector comprising the nucleic acid sequence of claim 54.

56. (New) A recombinant host cell comprising the vector of claim 55,

wherein said host cell is a hematopoietic stem cell.

57. (New) An inhibitor compound capable of inhibiting the transcription product or polypeptide encoded by at least one murine genomic region listed in claim 52 or its human homologue or capable of inhibiting the transcription product or polypeptide the expression of which is affected by a transformation in said genomic regions, wherein said inhibitor compound is an antibody or derivative thereof directed against said polypeptide, and wherein said polypeptide is expressed on the cell membrane.

58. (New) An inhibitor compound according to claim 57, wherein said derivative is selected from the group consisting of scFv fragments, Fab fragments, chimeric antibodies, bifunctional antibodies, intrabodies, other antibody-derived molecules, an antisense molecule, an RNAi molecule, a ribozyme and a small molecule interfering with the biological activity of said polypeptide.

59. (New) An inhibitor compound according to claim 57, for use in the treatment of acute myeloid leukemia (AML).

60. (New) A method of making a pharmaceutical composition for the treatment of cancer, comprising admixing an inhibitor compound according to claim 57 with at least one pharmaceutically acceptable excipient.

61. (New) The method according to claim 60, wherein the inhibitor is incorporated in an amount effective to treat an indication for which gene therapy is indicated.

62. (New) The method according to claim 60, wherein the inhibitor is selected for the treatment of inflammatory diseases.

63. (New) A pharmaceutical composition for the treatment of cancer, comprising at least one inhibitor compound according to claim 57 and a suitable excipient, carrier or diluent.

64. (New) A method of treating a mammal, comprising administering to a mammal the pharmaceutical composition of claim 63 in an amount effective to alleviate or prevent the formation of cancer.

65. (New) A method of treating a mammal, comprising administering to a mammal the hematopoietic stem cell of claim 56 in an amount effective to alleviate or prevent the formation of acute myeloid leukemia.

66. (New) A method of using of at least one murine genomic region listed in claim 52 or its human homologue or a transcription product thereof or polypeptide encoded thereby for the preparation of a diagnostic reagent for diagnosis of cancer.

67. (New) A diagnostic reagent capable of specifically binding to a murine genomic region listed in claim 52 or its human homologue or a transcription product thereof or polypeptide encoded thereby.

68. (New) A diagnostic composition comprising a diagnostic reagent according to claim 67.

69. (New) A method of using a diagnostic composition according to claim 68, for the diagnosis of cancer selected from the group consisting of solid tumor of lung, colon, breast, prostate, ovarian and acute myeloid leukemia (AML).

70. (New) A method of using a diagnostic composition according to claim 69, wherein the diagnosis is performed by means of histological analysis of tissue specimens using specific antibodies directed against encoded polypeptides, using in situ hybridisation

analysis of gene expression levels in tissue specimens with RNA probes directed against gene sequences or using polynucleotide or oligonucleotide arrays.

71. (New) A kit comprising diagnostic composition according to claim 68, and one or more reagents selected from the group consisting of reagents for the isolation of nucleic acid fragments from a sample, reagents for the isolation of polypeptides from a sample, reagents for immunostaining of a sample, reagents for in situ hybridisation of a sample and reagents for performing nucleic acid array hybridisations.

72. (New) A method for the development of an inhibitor compound according to 57, comprising the steps of:

- a) identification of genes involved in cancer;
- b) validation of one or more of the identified genes as potential target gene(s) for the inhibitor compound by one or more of the following methods:
  - confirmation of the identified gene by Northern Blot analysis in cancer cell-lines;
  - determination of the expression profile of the identified gene in tumors and normal tissue;
  - determination of the functional importance of the identified genes for cancer;
- c) production of the expression product of the gene; and
- d) use of the expression product of the gene for the production or design of an inhibitor compound.

73. (New) A method for the identification of genomic regions involved in the development of cancer comprising the steps of:

- a) performing retroviral insertional mutagenesis of a subject, comprising infecting said subject with a tumor inducing retrovirus;
- b) isolating chromosomal DNA from tumors developed in the infected subject;
- c) digesting said chromosomal DNA with a restriction enzyme capable of cutting at least once in the DNA sequence of said tumor inducing retrovirus and at least once in the chromosomal DNA of said subject;

- d) ligating the digested DNA to circular DNA;
- e) amplifying the chromosomal DNA fragment flanking the retroviral DNA sequence by performing a first PCR reaction with said circular DNA using a first set of retrovirus-specific primers and performing a second nested PCR with the product of said first PCR reaction using a second nested set of retrovirus-specific primers, and
- f) directly determining the nucleotide sequence of said chromosomal DNA fragment, and optionally comparing said nucleotide sequences with known sequences in a database to yield the genomic region involved in the development of cancer.

74. (New) A method for the identification of common virus integration sites in the development of cancer comprising the steps of

- a) performing the method of claim 73;
- b) designing genomic region-specific amplification primers;
- c) isolating nucleic acids from at least two tumors to be analysed for the presence of a common virus integration site;
- d) performing an amplification reaction with said nucleic acids using a set of nested primers comprising genomic region-specific primers and retrovirus-specific primers, and
- e) blotting the amplification products and separately hybridizing the resulting blot with a retrovirus-specific probe and a genomic region-specific probe to determine the presence of common virus integration sites between said tumors.

75. (New) A set of genomic regions obtainable by a method according to claim 74, wherein said genomic regions comprise at least 2 murine genomic regions selected from the group consisting of Adam11, Akap7, Arpgap14, Bomb, Cd24a, Cish2, Cig5, Clic3, Cra, Dermol, EMILIN, Flj20489, Galnt5, Hook, Ier5, IL16, Iprg1, Itgp, Kenk5, Irrc2, Ltb, Mbl1, Mrc1, Mtap7, Ninj2, Nr1d1, Pcdh9, Prdx2, Prps1, Pdi1, Ptgd3, Rgl1, Sardh, Scya4, Slc16A6, Swap70, Txnip, Trim46, Tnfrsf17 and Ub13., more preferably comprising at least 2, murine genomic regions selected from the group consisting of Cd24a, Cish2, Cra, Ltb and Prdx2.